

SEQUENCE LISTING

<110> MUSC Foundation For Research Development

<120> Complement Receptor 2 Targeted
Complement Modulators

<130> 19113.0095P1

<150> 60/426,676

<151> 2002-11-15

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1041

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

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gactgtggcc ttccccaga tgtaccta at gccagccag ctttgaagg ccgtacaagt 60
tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga agagtctctgc 180
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
actcagaatt attttccagt cgttactgtt gtggaatatg agtgccgtcc aggttacaga 300
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 420
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtac 480
aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 540
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 600
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcattgta 660
aaaggattca ccatgattgg agagcactct atttattgta ctgtgaataa tgatgaagga 720
gagtggagtg gccaccacc tgaatgcaga ggaaaatctc taacttccaa ggtcccacca 780
acagttcaga aacctaccac agtaaatgtt ccaactacag aagtctcacc aacttctcag 840
aaaaccacca caaaaaccac cacaccaa at gctcaagcaa cacggagtag acctgtttcc 900
aggacaacca agcattttca tgaaacaacc ccaaataaag gaagtggac cacttcaggt 960
actaccgctc ttctatctgg gcacacgtgt ttcacgttga cagggtttgt tgggacgcta 1020
gtaaccatgg gcttgetgac t                                     1041

```

<210> 2

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 2

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Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
1           5           10           15
Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val
20           25           30

```

```

Trp Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu
    35          40          45
Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys
    50          55          60
Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys
    65          70          75          80
Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser
    85          90          95
Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr
    100          105          110
Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys
    115          120          125
Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys
    130          135          140
Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys
    145          150          155          160
Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro
    165          170          175
Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly
    180          185          190
Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser
    195          200          205
Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys
    210          215          220
Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp
    225          230          235          240
His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe
    245          250          255
Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu
    260          265          270
Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr
    275          280          285
Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro
    290          295          300
Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr
    305          310          315          320
Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr
    325          330          335
Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser
    340          345          350
Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly
    355          360          365
Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
    370          375          380

```

<210> 3

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3

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cagtgtctaca actgtctctaa cccaactgct gactgcaaaa cagccgtcaa ttgttcatct 60
gattttgatg cgtgtctcat taccaaagct gggttacaag tgtataacaa gtgttggaag 120
tttgagcatt gcaatttcaa cgacgtcaca acccgcttga gggaaaatga gctaacgtac 180
tactgtctgca agaaggacct gtgtaacttt aacgaacagc ttgaaaatgg tgggacatcc 240
ttatcagaga aaacagttct tctgctggtg actccatttc tggcagcagc ctggagcctt 300

```

catccc

306

<210> 4

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 4

```

Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu
 1             5             10             15
Ala Val Phe Cys His Ser Gly His Gln Cys Tyr Asn Cys Pro Asn Pro
      20             25             30
Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe Asp Ala
      35             40             45
Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys
      50             55             60
Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg Glu Asn
      65             70             75             80
Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu
      85             90             95
Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val Leu Leu
      100             105             110
Leu Val Thr Pro Phe Leu Ala Ala Trp Ser Leu His Pro
      115             120             125

```

<210> 5

<211> 1485

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

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atttcttggtg gctctcctcc gcctatccta aatggccgga ttagttatta ttctaccccc 60
attgctggttg gtaccgtgat aaggtacagt tgttcaggta ccttccgcct cattggagaa 120
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctggt tgggtgcaag caaataatat gtggggggccg 360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatggt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctggtta cttgcttggt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc ccccatatgt gaagaggcac gctgtaaatc tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaatctt 660
ttctgtgatg aagggtatcg actgcaaggg ccaccttcta gtcggtgtgt aattgctgga 720
cagggagttg cttggaccaa aatgccagta tgtggaggtg ggtcgggtgg cggcggatcc 780
gactgtggcc ttccccaga tgtacctaat gccagccag ctttgggaagg ccgtacaagt 840
tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 900
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga agagtctgc 960
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat cctcaaaca gccttatatc 1020
actcagaatt attttccagt cggtaactgt gtggaatatg agtgccgtcc aggttacaga 1080
agagaacctt ctctatcacc aaaactaact tgcttcaga atttaaaatg gtccacagca 1140
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 1200
gatgtaccag gtggcatatt atttgggtgca accatctcct tctcatgtaa cacagggtac 1260

```

aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 1320
gaccggttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 1380
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcattgta 1440
aaaggattca ccatgattgg agagcactct atttattgta ctgtg 1485

<210> 6

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 6

Ile	Ser	Cys	Gly	Ser	Pro	Pro	Pro	Ile	Leu	Asn	Gly	Arg	Ile	Ser	Tyr
1				5					10					15	
Tyr	Ser	Thr	Pro	Ile	Ala	Val	Gly	Thr	Val	Ile	Arg	Tyr	Ser	Cys	Ser
			20					25					30		
Gly	Thr	Phe	Arg	Leu	Ile	Gly	Glu	Lys	Ser	Leu	Leu	Cys	Ile	Thr	Lys
		35					40					45			
Asp	Lys	Val	Asp	Gly	Thr	Trp	Asp	Lys	Pro	Ala	Pro	Lys	Cys	Glu	Tyr
		50				55					60				
Phe	Asn	Lys	Tyr	Ser	Ser	Cys	Pro	Glu	Pro	Ile	Val	Pro	Gly	Gly	Tyr
					70					75				80	
Lys	Ile	Arg	Gly	Ser	Thr	Pro	Tyr	Arg	His	Gly	Asp	Ser	Val	Thr	Phe
				85					90					95	
Ala	Cys	Lys	Thr	Asn	Phe	Ser	Met	Asn	Gly	Asn	Lys	Ser	Val	Trp	Cys
				100					105					110	
Gln	Ala	Asn	Asn	Met	Trp	Gly	Pro	Thr	Arg	Leu	Pro	Thr	Cys	Val	Ser
		115					120						125		
Val	Phe	Pro	Leu	Glu	Cys	Pro	Ala	Leu	Pro	Met	Ile	His	Asn	Gly	His
		130					135					140			
His	Thr	Ser	Glu	Asn	Val	Gly	Ser	Ile	Ala	Pro	Gly	Leu	Ser	Val	Thr
					150					155				160	
Tyr	Ser	Cys	Glu	Ser	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Lys	Ile	Ile	Asn
				165					170					175	
Cys	Leu	Ser	Ser	Gly	Lys	Trp	Ser	Ala	Val	Pro	Pro	Thr	Cys	Glu	Glu
				180				185					190		
Ala	Arg	Cys	Lys	Ser	Leu	Gly	Arg	Phe	Pro	Asn	Gly	Lys	Val	Lys	Glu
		195					200					205			
Pro	Pro	Ile	Leu	Arg	Val	Gly	Val	Thr	Ala	Asn	Phe	Phe	Cys	Asp	Glu
		210				215					220				
Gly	Tyr	Arg	Leu	Gln	Gly	Pro	Pro	Ser	Ser	Arg	Cys	Val	Ile	Ala	Gly
				230						235				240	
Gln	Gly	Val	Ala	Trp	Thr	Lys	Met	Pro	Val	Cys	Gly	Gly	Gly	Ser	Gly
				245					250					255	
Gly	Gly	Gly	Ser	Asp	Cys	Gly	Leu	Pro	Pro	Asp	Val	Pro	Asn	Ala	Gln
			260					265					270		
Pro	Ala	Leu	Glu	Gly	Arg	Thr	Ser	Phe	Pro	Glu	Asp	Thr	Val	Ile	Thr
		275					280					285			
Tyr	Lys	Cys	Glu	Glu	Ser	Phe	Val	Lys	Ile	Pro	Gly	Glu	Lys	Asp	Ser
		290				295					300				
Val	Ile	Cys	Leu	Lys	Gly	Ser	Gln	Trp	Ser	Asp	Ile	Glu	Glu	Phe	Cys
				310						315				320	
Asn	Arg	Ser	Cys	Glu	Val	Pro	Thr	Arg	Leu	Asn	Ser	Ala	Ser	Leu	Lys
				325					330					335	
Gln	Pro	Tyr	Ile	Thr	Gln	Asn	Tyr	Phe	Pro	Val	Gly	Thr	Val	Val	Glu
			340					345				350			
Tyr	Glu	Cys	Arg	Pro	Gly	Tyr	Arg	Arg	Glu	Pro	Ser	Leu	Ser	Pro	Lys
		355					360					365			

```

Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys
  370                375                380
Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile
 385                390                395                400
Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys
                405                410                415
Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile
                420                425                430
Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu
                435                440                445
Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly
 450                455                460
Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn
 465                470                475                480
Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val
                485                490                495

```

<210> 7

<211> 1002

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 7

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atttcttgtg gctctcctcc gcctatccta aatggcggga ttagttatta ttctaccccc 60
attgctgttg gtaccgtgat aaggtacagt tgttcaggta ccttcgcct cattggagaa 120
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctgtt tgggtgcaag caaataatat gtggggggcgg 360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctgggta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc cccacatgt gaagaggcac gctgtaaatc tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 660
ttctgtgatg aagggatcgc actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
cagggagttg cttggaccaa aatgccagta tgttcaggag gaggagggtc cctgcagtgc 780
tacaactgtc ctaacccaac tgctgactgc aaaacagccg tcaattgttc atctgatttt 840
gatgcgtgtc tcattaccaa agctgggtta caagtgtata acaagtgttg gaagtttgag 900
cattgcaatt tcaacgacgt cacaacccgc ttgagggaaa atgagctaac gtactactgc 960
tgcaagaagg acctgtgtaa cttaacgaa cagcttgaaa at 1002

```

<210> 8

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 8

```

Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr
  1                5                10                15
Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
                20                25                30

```

Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
 35 40 45
 Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
 50 55 60
 Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
 65 70 75 80
 Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
 85 90 95
 Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
 100 105 110
 Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
 115 120 125
 Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
 130 135 140
 His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
 145 150 155 160
 Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
 165 170 175
 Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu
 180 185 190
 Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu
 195 200 205
 Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu
 210 215 220
 Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly
 225 230 235 240
 Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Ser Gly Gly Gly Gly
 245 250 255
 Ser Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr
 260 265 270
 Ala Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala
 275 280 285
 Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe
 290 295 300
 Asn Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys
 305 310 315 320
 Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn
 325 330

<210> 9

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 9

gactgtggcc ttccccccaga tgtacctaat gccccagccag ctttggaagg ccgtacaagt 60
 tttcccagagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120
 gagaaggact cagtgatctg ccttaagggc agtcaatggg cagatattga agagttctgc 180
 aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
 actcagaatt attttccagt cggtactgtt gtggaatatg agtgccgtcc aggttacaga 300
 agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360
 gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 420
 gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtag 480
 aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 540
 gaccggttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 600
 ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcagttaat 660

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aaaggattca ccatgattgg agagcactct atttattgta ctgtgaataa tgatgaagga 720
gagtggagtg gccaccacc tgaatgcaga tcctctggtg gcggtggctc gggcggaggt 780
gggtcgggtg gcggcggatc catttcttgt ggctctcctc cgcctatcct aaatggccgg 840
attagttatt attctacccc cattgctgtt ggtaccgtga taaggtacag ttgttcaggt 900
accttccgcc tcattggaga aaaaagtcta ttatgcataa ctaaagacaa agtggatgga 960
acctgggata aacctgctcc taaatgtgaa ttttcaata aatattcttc ttgccctgag 1020
cccatagtag caggaggata caaaattaga ggctctacac cctacagaca tggtgattct 1080
gtgacatttg cctgtaaaac caacttctcc atgaacggaa acaagtctgt ttggtgtcaa 1140
gcaaataata tgtggggggc gacacgacta ccaacctgtg taagtgtttt ccctctcgag 1200
tgtccagcac ttcctatgat ccacaatgga catcacacaa gtgagaatgt tggctccatt 1260
gctccaggat tgtctgtgac ttacagctgt gaatctggtt acttgcttgt tggagaaaag 1320
atcattaact gtttgtcttc gggaaaatgg agtgcgtgcc cccccacatg tgaagaggca 1380
cgctgtaaat ctctaggacg atttcccaat gggaaggtaa aggagcctcc aattctccgg 1440
gttggtgtaa ctgcaaaact tttctgtgat gaagggtatc gactgcaagg cccaccttct 1500
agtcgggtgtg taattgctgg acaggggagt gcttggacca aaatgccagt atgt 1554

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<210> 10

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 10

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Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu
1      5      10      15
Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu
20     25     30
Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu
35     40     45
Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys
50     55     60
Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile
65     70     75     80
Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg
85     90     95
Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu
100    105    110
Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys Ser
115    120    125
Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly
130    135    140
Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr
145    150    155    160
Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser
165    170    175
Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro
180    185    190
Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His
195    200    205
Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr
210    215    220
Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly
225    230    235    240
Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Ser Ser Gly Gly Gly Gly
245    250    255
Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Ser Cys Gly Ser
260    265    270

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Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr Tyr Ser Thr Pro Ile
 275 280 285
 Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser Gly Thr Phe Arg Leu
 290 295 300
 Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys Asp Lys Val Asp Gly
 305 310 315 320
 Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr Phe Asn Lys Tyr Ser
 325 330 335
 Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr Lys Ile Arg Gly Ser
 340 345 350
 Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe Ala Cys Lys Thr Asn
 355 360 365
 Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys Gln Ala Asn Asn Met
 370 375 380
 Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser Val Phe Pro Leu Glu
 385 390 395 400
 Cys Pro Ala Leu Pro Met Ile His Asn Gly His His Thr Ser Glu Asn
 405 410 415
 Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr Tyr Ser Cys Glu Ser
 420 425 430
 Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu Ser Ser Gly
 435 440 445
 Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu Ala Arg Cys Lys Ser
 450 455 460
 Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu Pro Pro Ile Leu Arg
 465 470 475 480
 Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu Gly Tyr Arg Leu Gln
 485 490 495
 Gly Pro Pro Ser Arg Cys Val Ile Ala Gly Gln Gly Val Ala Trp
 500 505 510
 Thr Lys Met Pro Val Cys
 515

<210> 11

<211> 990

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 11

ctgcagtgtct acaactgtcc taaccaact gctgactgca aaacagccgt caattgttca 60
 tctgattttg atgcgtgtct cattaccaa gctgggttac aagtgtataa caagtgttg 120
 aagtttgagc attgcaattt caacgacgtc acaaccgct tgagggaaaa tgagctaacg 180
 tactactgct gcaagaagga cctgtgtaac ttttaacgaac agcttgaaaa ttcctctggt 240
 ggcggtggct ccggcggagg tgggtccggt ggcggcggat ccatttcttg tggctctcct 300
 ccgcctatcc taaatggccg gattagttat tattctaccc ccattgctgt tggtagcgtg 360
 ataaggtaca gttgttcagg taccttccgc ctcatggag aaaaaagtct attatgcata 420
 actaaagaca aagtggatgg aacctgggat aaacctgctc cttaatgtga atatttcaat 480
 aaatattctt cttgccctga gccatagta ccaggaggat acaaaattag aggctctaca 540
 ccctacagac atgggtgattc tgtgacattt gcctgtaaaa ccaacttctc catgaacgga 600
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 tacttgcttg ttggagaaaa gatcattaac tgtttgtctt cgggaaaaatg gagtgctgtc 840
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<210> 12
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 12
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 Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
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 Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
 35 40 45
 Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
 50 55 60
 Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Ser Ser Gly
 65 70 75 80
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Ser
 85 90 95
 Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr Tyr Ser
 100 105 110
 Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser Gly Thr
 115 120 125
 Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys Asp Lys
 130 135 140
 Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr Phe Asn
 145 150 155 160
 Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr Lys Ile
 165 170 175
 Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe Ala Cys
 180 185 190
 Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys Gln Ala
 195 200 205
 Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser Val Phe
 210 215 220
 Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His His Thr
 225 230 235 240
 Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr Tyr Ser
 245 250 255
 Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu
 260 265 270
 Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu Ala Arg
 275 280 285
 Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu Pro Pro
 290 295 300
 Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu Gly Tyr
 305 310 315 320
 Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
 325 330

<210> 13
 <211> 5994
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 13

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<210> 14

<211> 2048

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 14

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Val Gly Pro Pro Ala Pro Gly Leu Pro Phe Cys Cys Gly Gly Ser Leu
          20            25            30

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 35 40 45
 Asn Ala Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr
 50 55 60
 Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr
 65 70 75 80
 Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu
 85 90 95
 Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser
 100 105 110
 Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys
 115 120 125
 Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr
 130 135 140
 Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr
 145 150 155 160
 Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly
 165 170 175
 Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 180 185 190
 Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 195 200 205
 Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 210 215 220
 Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
 225 230 235 240
 Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
 245 250 255
 Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
 260 265 270
 Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
 275 280 285
 Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
 290 295 300
 Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
 305 310 315 320
 Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
 325 330 335
 Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
 340 345 350
 Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
 355 360 365
 Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
 370 375 380
 Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
 385 390 395 400
 Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 405 410 415
 Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 420 425 430
 Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 435 440 445
 Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 450 455 460
 Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 465 470 475 480
 Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 485 490 495
 Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 500 505 510

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
 515 520 525
 Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
 530 535 540
 Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
 545 550 555 560
 Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
 565 570 575
 Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 580 585 590
 Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
 595 600 605
 Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro
 610 615 620
 Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn
 625 630 635 640
 Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro
 645 650 655
 Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
 660 665 670
 Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
 675 680 685
 Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
 690 695 700
 Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
 705 710 715 720
 Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
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 Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
 740 745 750
 Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr
 755 760 765
 Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
 770 775 780
 Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr
 785 790 795 800
 Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser
 805 810 815
 Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro
 820 825 830
 Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly
 835 840 845
 Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met
 850 855 860
 Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys
 865 870 875 880
 Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu
 885 890 895
 Glu Val Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His
 900 905 910
 Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg
 915 920 925
 Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
 930 935 940
 Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe
 945 950 955 960
 Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr
 965 970 975
 Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser
 980 985 990

Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys
 995 1000 1005
 Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val
 1010 1015 1020
 His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys
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 Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu
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 Ser Gly Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg
 1060 1065 1070
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 1075 1080 1085
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 1090 1095 1100
 Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro
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 Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly
 1125 1130 1135
 Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val
 1140 1145 1150
 Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn
 1155 1160 1165
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 Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val
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 Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu
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 Phe Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp
 1285 1290 1295
 Glu Gly Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val
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 1330 1335 1340
 Pro Ser Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp
 1345 1350 1355 1360
 Pro His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr
 1365 1370 1375
 Ile Arg Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro
 1380 1385 1390
 Ala Pro Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro
 1395 1400 1405
 Glu Gln Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu
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 Phe Pro Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe
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 Gly Lys Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser
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 1460 1465 1470

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 Val Asn Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile Gly Ser Pro Ser
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 Val Thr Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu
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 1585 1590 1595 1600
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 Phe Phe Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe
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 Val Met Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg Trp
 1635 1640 1645
 Gly Pro Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro Pro Glu
 1650 1655 1660
 Ile Leu His Gly Glu His Thr Leu Ser His Gln Asp Asn Phe Ser Pro
 1665 1670 1675 1680
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 1685 1690 1695
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 Pro Arg Cys Thr Val Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro
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 His Gly Arg Val Leu Leu Pro Leu Asn Leu Gln Leu Gly Ala Lys Val
 1730 1735 1740
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 1745 1750 1755 1760
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 1765 1770 1775
 Val Cys Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly
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 1795 1800 1805
 Ser Tyr Ala Cys Asp Thr His Pro Asp Arg Gly Met Thr Phe Asn Leu
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 Ile Gly Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly
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 Val Trp Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val Pro Ala Ala
 1845 1850 1855
 Cys Pro His Pro Pro Lys Ile Gln Asn Gly His Tyr Ile Gly Gly His
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 Gly Tyr Leu Leu Val Gly Lys Gly Phe Ile Phe Cys Thr Asp Gln Gly
 1890 1895 1900
 Ile Trp Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn Cys Ser Phe
 1905 1910 1915 1920
 Pro Leu Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met Lys Lys Val
 1925 1930 1935
 Tyr His Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp Gly Tyr Thr
 1940 1945 1950

Leu Glu Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp
 1955 1960 1965
 Pro Pro Leu Ala Lys Cys Thr Ser Arg Ala His Asp Ala Leu Ile Val
 1970 1975 1980
 Gly Thr Leu Ser Gly Thr Ile Phe Phe Ile Leu Leu Ile Ile Phe Leu
 1985 1990 1995 2000
 Ser Trp Ile Ile Leu Lys His Arg Lys Gly Asn Asn Ala His Glu Asn
 2005 2010 2015
 Pro Lys Glu Val Ala Ile His Leu His Ser Gln Gly Gly Ser Ser Val
 2020 2025 2030
 His Pro Arg Thr Leu Gln Thr Asn Glu Glu Asn Ser Arg Val Leu Pro
 2035 2040 2045

<210> 15

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 15

tgtgaggagc caccaacatt tgaagctatg gagctcattg gtaaaccaaa accctactat 60
 gagattggtg aacgagtaga ttataagtgt aaaaaaggat acttctatat acctcctctt 120
 gccacccata ctatttgtga tcggaatcat acatggctac ctgtctcaga tgacgcctgt 180
 tatagagaaa catgtccata tatacgggat cctttaaatg gccaaagcagt ccctgcaaat 240
 gggacttacg agtttggtta tcagatgcac tttatttgta atgaggggta ttacttaatt 300
 ggtgaagaa ttctatatg tgaacttaaa ggatcagtag caatttggag cggtaagccc 360
 ccaatatgtg aaaaggtttt gtgtacacca cctccaaaaa taaaaaatgg aaaacacacc 420
 tttagtgaag tagaagtatt tgagtatctt gatgcagtaa cttatagttg tgatcctgca 480
 cctggaccag atccattttc acttattgga gagagcacga tttattgtgg tgacaattca 540
 gtgtggagtc gtgctgctcc agagtgtaaa gtggtcaaat gtcgatttcc agtagtcgaa 600
 aatggaaaac agatatcagg atttggaana aaattttact acaaagcaac agttatgttt 660
 gaatgcgata agggttttta cctcgatggc agcgacacaa ttgtctgtga cagtaacagt 720
 acttgggata ccccatgtcc aaagtgtcgt aaagtgtcga cttcttccac tacaaaatct 780
 ccagcgtcca gtgcctcagg tcctaggcct acttacaagc ctccagtctc aaattatcca 840
 ggatatccta aacctgagga aggaatactt gacagtttgg atgtttgggt cattgctgtg 900
 attgttattg ccatagttgt tggagttgca gtaatttgtg ttgtcccgtg cagatatctt 960
 caaaggagga agaagaaagg cacataccta actgatgaga cccacagaga agtaaaaattt 1020
 acttctctc 1029

<210> 16

<211> 378

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 16

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
 1 5 10 15
 Phe Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe
 20 25 30
 Ser Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile
 35 40 45
 Gly Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys
 50 55 60

Cys Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile
 65 70 75 80
 Cys Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr
 85 90 95
 Arg Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val
 100 105 110
 Pro Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys
 115 120 125
 Asn Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu
 130 135 140
 Lys Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Ile Cys Glu Lys
 145 150 155 160
 Val Leu Cys Thr Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe
 165 170 175
 Ser Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys
 180 185 190
 Asp Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr
 195 200 205
 Ile Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys
 210 215 220
 Lys Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile
 225 230 235 240
 Ser Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu
 245 250 255
 Cys Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp
 260 265 270
 Ser Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser
 275 280 285
 Thr Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg
 290 295 300
 Pro Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro
 305 310 315 320
 Glu Glu Gly Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile
 325 330 335
 Val Ile Ala Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr
 340 345 350
 Arg Tyr Leu Gln Arg Arg Lys Lys Gly Thr Tyr Leu Thr Asp Glu
 355 360 365
 Thr His Arg Glu Val Lys Phe Thr Ser Leu
 370 375

<210> 17

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 17

Met Glu Val Ser Ser Arg Ser Ser Glu Pro Leu Asp Pro Val Trp Leu
 1 5 10 15
 Leu Val Ala Phe Gly Arg Gly Gly Val Lys Leu Glu Val Leu Leu Leu
 20 25 30
 Phe Leu Leu Pro Phe Thr Leu Gly His Cys Pro Ala Pro Ser Gln Leu
 35 40 45
 Pro Ser Ala Lys Pro Ile Asn Leu Thr Asp Glu Ser Met Phe Pro Ile
 50 55 60

Gly Thr Tyr Leu Leu Tyr Glu Cys Leu Pro Gly Tyr Ile Lys Arg Gln
 65 70 75 80
 Phe Ser Ile Thr Cys Lys Gln Asp Ser Thr Trp Thr Ser Ala Glu Asp
 85 90 95
 Lys Cys Ile Arg Lys Gln Cys Lys Thr Pro Ser Asp Pro Glu Asn Gly
 100 105 110
 Leu Val His Val His Thr Gly Ile Gln Phe Gly Ser Arg Ile Asn Tyr
 115 120 125
 Thr Cys Asn Gln Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Val Cys
 130 135 140
 Val Ile Thr Asp Gln Ser Val Asp Trp Asp Thr Glu Ala Pro Ile Cys
 145 150 155 160
 Glu Trp Ile Pro Cys Glu Ile Pro Pro Gly Ile Pro Asn Gly Asp Phe
 165 170 175
 Phe Ser Ser Thr Arg Glu Asp Phe His Tyr Gly Met Val Val Thr Tyr
 180 185 190
 Arg Cys Asn Thr Asp Ala Arg Gly Lys Ala Leu Phe Asn Leu Val Gly
 195 200 205
 Glu Pro Ser Leu Tyr Cys Thr Ser Asn Asp Gly Glu Ile Gly Val Trp
 210 215 220
 Ser Gly Pro Pro Pro Gln Cys Ile Glu Leu Asn Lys Cys Thr Pro Pro
 225 230 235 240
 Pro Tyr Val Glu Asn Ala Val Met Leu Ser Glu Asn Arg Ser Leu Phe
 245 250 255
 Ser Leu Arg Asp Ile Val Glu Phe Arg Cys His Pro Gly Phe Ile Met
 260 265 270
 Lys Gly Ala Ser Ser Val His Cys Gln Ser Leu Asn Lys Trp Glu Pro
 275 280 285
 Glu Leu Pro Ser Cys Phe Lys Gly Val Ile Cys Arg Leu Pro Gln Glu
 290 295 300
 Met Ser Gly Phe Gln Lys Gly Leu Gly Met Lys Lys Glu Tyr Tyr Tyr
 305 310 315 320
 Gly Glu Asn Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly
 325 330 335
 Ser Ser Gln Ser Gln Cys Gln Ser Asp Gly Ser Trp Asn Pro Leu Leu
 340 345 350
 Ala Lys Cys Val Ser Arg Ser Ile Ser Gly Leu Ile Val Gly Ile Phe
 355 360 365
 Ile Gly Ile Ile Val Phe Ile Leu Val Ile Ile Val Phe Ile Trp Met
 370 375 380
 Ile Leu Lys Tyr Lys Lys Arg Asn Thr Thr Asp Glu Lys Tyr Lys Glu
 385 390 395 400
 Val Gly Ile His Leu Asn Tyr Lys Glu Asp Ser Cys Val Arg Leu Gln
 405 410 415
 Ser Leu Leu Thr Ser Gln Glu Asn Ser Ser Thr Thr Ser Pro Ala Arg
 420 425 430
 Asn Ser Leu Thr Gln Glu Val Ser
 435 440

<210> 18

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 18

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Pro Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 19

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 19

Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn
 1 5 10 15
 Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp
 20 25 30
 Phe Leu Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser
 35 40 45
 Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys
 50 55 60
 Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln
 65 70 75 80
 Gly Thr Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn
 85 90 95
 Lys Glu Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys
 100 105 110
 Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg
 115 120 125
 Ser Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln
 130 135 140

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Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val
145          150          155          160
Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr
          165          170
Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser
          180          185          190
Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln
          195          200          205
Gln Asn Ala Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg
          210          215          220
Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser
225          230          235          240
Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val
          245          250          255
Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr
          260          265          270
Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu
          275          280          285
Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys
          290          295          300
Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser
305          310          315          320
Arg Pro Lys Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro
          325          330          335
Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys
          340          345          350
Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln
          355          360          365
Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met
          370          375          380
Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr
385          390          395          400
Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val
          405          410          415
Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys
          420          425          430
Ser Thr Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp
          435          440          445
Thr Ala Gly Thr Cys Tyr
          450

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<210> 20

<211> 1530

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 20

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atgggcgcgcg cgggcctgct cgggggttttc ttggtctctcg tcgcaccggg ggtcctcggg 60
atttcttggtg gctctctctcc gcctataccta aatggccgga ttagttatta ttctaccccc 120
attgctgttg gtaccgtgat aaggtacagt tgttcaggta ccttcgcct cattggagaa 180
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 240
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 300
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 360
aacttctcca tgaacggaaa caagtctgtt tgggtgtcaag caaataatat gtgggggccc 420
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 480
cacaatggac atcacacaag tgagaatggt ggctccattg ctccaggatt gtctgtgact 540

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tacagctgtg aatctggtta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 600
ggaaaatgga gtgctgtccc cccacatgt gaagaggcac gctgtaaactc tctaggacga 660
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 720
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 780
cagggagttg cttggaccaa aatgccagta tgtgaagaaa ttttttgccc actgcggccg 840
cagctctagag acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 900
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 960
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 1020
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 1080
agcacgtacc gtgtggtcag cgctctcacc gtcctgcacc aggactggct gaatggcaag 1140
gagtacaagt gcaaggtctc caacaaagcc ctcccagtc ccatcgagaa aaccatctcc 1200
aaagccaaag ggcagccccc agaaccacag gtgtacaccc tgccccatc ccgggaggag 1260
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1320
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1380
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1440
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1500
cagaagagcc tctccctgtc cccgggtaaa 1530

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<210> 21

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 21

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Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro
1           5           10           15
Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly
20           25           30
Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
35           40           45
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
50           55           60
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
65           70           75           80
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
85           90           95
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
100          105          110
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
115          120          125
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
130          135          140
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
145          150          155          160
His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
165          170          175
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
180          185          190
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
195          200          205
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
210          215          220
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
225          230          235          240
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
245          250          255

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Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
      260      265      270
Glu Ile Phe Cys Pro Leu Arg Pro Gln Ser Arg Asp Lys Thr His Thr
      275      280      285
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
      290      295      300
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
      305      310      315      320
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
      325      330      335
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
      340      345      350
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
      355      360      365
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
      370      375      380
Lys Val Ser Asn Lys Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser
      385      390      395      400
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
      405      410      415
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
      420      425      430
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
      435      440      445
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
      450      455      460
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
      465      470      475      480
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
      485      490      495
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
      500      505      510

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<210> 22

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 22

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Glu Pro Arg Ile Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro
1      5      10      15
Pro Gly Asn Ile Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
      20      25      30
Pro Lys Asp Ala Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val
      35      40      45
Val Val Asp Val Ser Glu Asp Asp Pro Asp Val His Val Ser Trp Phe
      50      55      60
Val Asp Asn Lys Glu Val His Thr Ala Trp Thr Gln Pro Arg Glu Ala
      65      70      75      80
Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Ala Leu Pro Ile Gln His
      85      90      95
Gln Asp Trp Met Arg Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
      100      105      110
Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Arg
      115      120      125

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Ala Gln Thr Pro Gln Val Tyr Thr Ile Pro Pro Pro Arg Glu Gln Met
 130 135 140
 Ser Lys Lys Lys Val Ser Leu Thr Cys Leu Val Thr Asn Phe Phe Ser
 145 150 155 160
 Glu Ala Ile Ser Val Glu Trp Glu Arg Asn Gly Glu Leu Glu Gln Asp
 165 170 175
 Tyr Lys Asn Thr Pro Pro Ile Leu Asp Ser Asp Gly Thr Tyr Phe Leu
 180 185 190
 Tyr Ser Lys Leu Thr Val Asp Thr Asp Ser Trp Leu Gln Gly Glu Ile
 195 200 205
 Phe Thr Cys Ser Val Val His Glu Ala Leu His Asn His His Thr Gln
 210 215 220
 Lys Asn Leu Ser Arg Ser Pro Gly Lys
 225 230

<210> 23

<211> 4860

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 23

gctctctaca ccctcatcac ccctgctggt ttgcgaacag acacagaaga gcaaattttg 60
 gtggaggccc atggagacag tactccaaaa cagcttgaca tctttgttca tgattttcca 120
 cggaagcaga aaaccttggt ccaaacacaga gtagatatga atccagcagg aggcattgctt 180
 gtcactccaa ctatagagat tccagcaaaa gaagtgaagta cggactccag gcaaaatcaa 240
 tatgtggttg tgcaagtaac tggctcctcaa gtgagattgg aaaaggtggt tctcctttct 300
 taccagagta gctttctggt tatccagaca gataaaggca tctatacacc agggctctcca 360
 gtactctatc gtgttttttc tatggatcac aacacaagca agatgaacaa aactgtgatt 420
 gttgagtttc agactccaga aggcattctt gtcagttcta attcagttga cctaaacttc 480
 ttctggcctt acaatttacc agacctgtgc agtttgggga cttggaggat tgtggccaaa 540
 tatgaacatt cccagagaga ttatactgca tattttgatg tcaggaaata tgtgttgcca 600
 agctttgaag tccgtctgca accatcagag aagttttttt acattgacgg caatgaaaat 660
 ttccacgtgt ctatcactgc aaggtacttg tatggagagg aagtggagg tgtggccttt 720
 gtctcttttg gactgaaaat agatgatgct aaaaagagta ttccagactc actcacgaga 780
 attccgatta ttgatggaga tgggaaagca acactaaaa gagatacatt ccgttctcga 840
 tttccaaatc tcaatgagct tgttgggcat actctgtatg catctgtaac agtcacgaca 900
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 ccattgaatg ctcaaagcct accaatcact gttagaacta accatggaga cctcccaaga 1200
 gaacgccagg caacaaagtc catgacagcc atagcctacc aaaccaggag aggatctgga 1260
 aactatcttc atgtagccat tacatctaca gagattaagc ccggagataa cttacctgtc 1320
 aatttcaatg tgaagggcaa tgcaaatcca ctgaagcaga tcaaatattt cacatacctc 1380
 atattgaata aagggaagat tttcaagggt ggcaggcaac ccaggagaga tgggcagaat 1440
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 tactaccaag tgggaaacaa cgaaattgtg gctgattctg tctgggtgga tgtgaaggat 1560
 acctgcatgg gaacgttggt tgtgaaagga gacaatctaa taaaaatgcc aggagctgca 1620
 atgaaaatca aattggaagg ggatccaggt gctcgggttg gtcttgtggc tgtggacaaa 1680
 gcagtatatg ttctcaatga taaatataag attagccaag ctaagatatg ggacacaata 1740
 gaaaagagtg actttggctg tacagctggc agtggccaga ataactctggg tgtgtttgaa 1800
 gatgctggac tggctctgac aaccagcact aatctcaaca ccaaacagag atcagctgca 1860
 aagtgtcctc agcctgcaaa tcggaggcgt cgcagttctg ttttgtctgt tgacagcaac 1920
 ggaaccaaaag cggcgaaatt tcaggatcaa gacctgcgta aatgctgtga agatgtcatg 1980
 catgagaacc ccatggggta cacttgtgaa aagcgtgcaa aatacatcca ggaggagat 2040
 gcttgtaagg ctgccttcct tgaatgctgt cgctacatca aggggggtccg agatgaaaac 2100

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caacgggaga gcgagttggt tctggcaaga gatgataatg aagatgggtt catagcagat 2160
agtgatatca tctcaagggtc tgatttcccc aagagttgggt tgtggctaac aaaggacttg 2220
accgaggagc ctaacagtcga agggattttca agcaagacaa tgtcttttta tctgagggat 2280
tccatcacaa cctgggtggt gctggctgta agctttacac ccaccaaagg gatctgtgtg 2340
gctgaacctt atgaaataag agtcatgaaa gtcttcttca ttgatcttca aatgccatat 2400
tcagtagtga agaattgagca ggtggagatt cgagctattc tgcacaacta cgttaacgag 2460
gatatttatg tgcgagtggg actgttatac aacccagcct tctgcagtgc ttccacaaaa 2520
ggacaaagat accgacagca gttcccaatt aaagccctgt cctccagagc agtaccgttt 2580
gtgatagtcc cattagagca aggattgcat gatgttgaga ttaaagcaag tgtccaggaa 2640
gcgttggtgt cagacgggtg gaggaagaaa ctgaaagttg tacctgaagg ggtacagaaa 2700
tccattgtga ctattgttaa actggaccca agggcaaaaag gagtgtgtgtg aacacagcta 2760
gaagtgatca aagcccgcga attagatgac agagtgcctg acacagaaat tgaaccaag 2820
attatcatcc aaggtgaccc tgtggctcag attattgaaa actcaattga tggaaagtaa 2880
ctcaaccatc tcattatcac tccttctggc tbtggggagc aaaatatgat ccgdatggcc 2940
gcaccagtta ttgccaccta ctacctggac accacagagc agtgggagac tctcggcata 3000
aatcgcagga ctgaagctgt caatcagatc gtgactgggt atgccagca gatggtgtac 3060
aagaaagcag atcattccta tgcagcattt acaaaccgtg catctagtcc ttggctaaca 3120
gcatatgtcg taaaagtctt tgccatggct gccaaaatgg tagcaggcat tagtcatgaa 3180
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aaagaaaatg cccctgtact ttctggaaca atgcagggag gaattcaagg tgctgaagaa 3300
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gatgttttag aagttattaa acaaggtact gacgaaaatc cagcagcaaa gacccaccag 4620
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aagaacacat ggattgagag atggccacat gaagacgaat gtcaggaaga agaattccaa 4800
aagttgtgtg atgactttgc tcagtttagc tacacattga ctgagtttgg ctgccctact 4860

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<210> 24

<211> 1620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 24

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1

5

10

15

Glu Gln Ile Leu Val Glu Ala His Gly Asp Ser Thr Pro Lys Gln Leu
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 Asp Ile Phe Val His Asp Phe Pro Arg Lys Gln Lys Thr Leu Phe Gln
 35 40 45
 Thr Arg Val Asp Met Asn Pro Ala Gly Gly Met Leu Val Thr Pro Thr
 50 55 60
 Ile Glu Ile Pro Ala Lys Glu Val Ser Thr Asp Ser Arg Gln Asn Gln
 65 70 75 80
 Tyr Val Val Val Gln Val Thr Gly Pro Gln Val Arg Leu Glu Lys Val
 85 90 95
 Val Leu Leu Ser Tyr Gln Ser Ser Phe Leu Phe Ile Gln Thr Asp Lys
 100 105 110
 Gly Ile Tyr Thr Pro Gly Ser Pro Val Leu Tyr Arg Val Phe Ser Met
 115 120 125
 Asp His Asn Thr Ser Lys Met Asn Lys Thr Val Ile Val Glu Phe Gln
 130 135 140
 Thr Pro Glu Gly Ile Leu Val Ser Ser Asn Ser Val Asp Leu Asn Phe
 145 150 155 160
 Phe Trp Pro Tyr Asn Leu Pro Asp Leu Val Ser Leu Gly Thr Trp Arg
 165 170 175
 Ile Val Ala Lys Tyr Glu His Ser Pro Glu Asn Tyr Thr Ala Tyr Phe
 180 185 190
 Asp Val Arg Lys Tyr Val Leu Pro Ser Phe Glu Val Arg Leu Gln Pro
 195 200 205
 Ser Glu Lys Phe Phe Tyr Ile Asp Gly Asn Glu Asn Phe His Val Ser
 210 215 220
 Ile Thr Ala Arg Tyr Leu Tyr Gly Glu Glu Val Glu Gly Val Ala Phe
 225 230 235 240
 Val Leu Phe Gly Val Lys Ile Asp Asp Ala Lys Lys Ser Ile Pro Asp
 245 250 255
 Ser Leu Thr Arg Ile Pro Ile Ile Asp Gly Asp Gly Lys Ala Thr Leu
 260 265 270
 Lys Arg Asp Thr Phe Arg Ser Arg Phe Pro Asn Leu Asn Glu Leu Val
 275 280 285
 Gly His Thr Leu Tyr Ala Ser Val Thr Val Met Thr Glu Ser Gly Ser
 290 295 300
 Asp Met Val Val Thr Glu Gln Ser Gly Ile His Ile Val Ala Ser Pro
 305 310 315 320
 Tyr Gln Ile His Phe Thr Lys Thr Pro Lys Tyr Phe Lys Pro Gly Met
 325 330 335
 Pro Tyr Glu Leu Thr Val Tyr Val Thr Asn Pro Asp Gly Ser Pro Ala
 340 345 350
 Ala His Val Pro Val Val Ser Glu Ala Phe His Ser Met Gly Thr Thr
 355 360 365
 Leu Ser Asp Gly Thr Ala Lys Leu Ile Leu Asn Ile Pro Leu Asn Ala
 370 375 380
 Gln Ser Leu Pro Ile Thr Val Arg Thr Asn His Gly Asp Leu Pro Arg
 385 390 395 400
 Glu Arg Gln Ala Thr Lys Ser Met Thr Ala Ile Ala Tyr Gln Thr Gln
 405 410 415
 Gly Gly Ser Gly Asn Tyr Leu His Val Ala Ile Thr Ser Thr Glu Ile
 420 425 430
 Lys Pro Gly Asp Asn Leu Pro Val Asn Phe Asn Val Lys Gly Asn Ala
 435 440 445
 Asn Ser Leu Lys Gln Ile Lys Tyr Phe Thr Tyr Leu Ile Leu Asn Lys
 450 455 460
 Gly Lys Ile Phe Lys Val Gly Arg Gln Pro Arg Arg Asp Gly Gln Asn
 465 470 475 480
 Leu Val Thr Met Asn Leu His Ile Thr Pro Asp Leu Ile Pro Ser Phe
 485 490 495

Arg Phe Val Ala Tyr Tyr Gln Val Gly Asn Asn Glu Ile Val Ala Asp
 500 505 510
 Ser Val Trp Val Asp Val Lys Asp Thr Cys Met Gly Thr Leu Val Val
 515 520 525
 Lys Gly Asp Asn Leu Ile Gln Met Pro Gly Ala Ala Met Lys Ile Lys
 530 535 540
 Leu Glu Gly Asp Pro Gly Ala Arg Val Gly Leu Val Ala Val Asp Lys
 545 550 555 560
 Ala Val Tyr Val Leu Asn Asp Lys Tyr Lys Ile Ser Gln Ala Lys Ile
 565 570 575
 Trp Asp Thr Ile Glu Lys Ser Asp Phe Gly Cys Thr Ala Gly Ser Gly
 580 585 590
 Gln Asn Asn Leu Gly Val Phe Glu Asp Ala Gly Leu Ala Leu Thr Thr
 595 600 605
 Ser Thr Asn Leu Asn Thr Lys Gln Arg Ser Ala Ala Lys Cys Pro Gln
 610 615 620
 Pro Ala Asn Arg Arg Arg Arg Ser Ser Val Leu Leu Leu Asp Ser Asn
 625 630 635 640
 Ala Ser Lys Ala Ala Glu Phe Gln Asp Gln Asp Leu Arg Lys Cys Cys
 645 650 655
 Glu Asp Val Met His Glu Asn Pro Met Gly Tyr Thr Cys Glu Lys Arg
 660 665 670
 Ala Lys Tyr Ile Gln Glu Gly Asp Ala Cys Lys Ala Ala Phe Leu Glu
 675 680 685
 Cys Cys Arg Tyr Ile Lys Gly Val Arg Asp Glu Asn Gln Arg Glu Ser
 690 695 700
 Glu Leu Phe Leu Ala Arg Asp Asp Asn Glu Asp Gly Phe Ile Ala Asp
 705 710 715 720
 Ser Asp Ile Ile Ser Arg Ser Asp Phe Pro Lys Ser Trp Leu Trp Leu
 725 730 735
 Thr Lys Asp Leu Thr Glu Glu Pro Asn Ser Gln Gly Ile Ser Ser Lys
 740 745 750
 Thr Met Ser Phe Tyr Leu Arg Asp Ser Ile Thr Thr Trp Val Val Leu
 755 760 765
 Ala Val Ser Phe Thr Pro Thr Lys Gly Ile Cys Val Ala Glu Pro Tyr
 770 775 780
 Glu Ile Arg Val Met Lys Val Phe Phe Ile Asp Leu Gln Met Pro Tyr
 785 790 795 800
 Ser Val Val Lys Asn Glu Gln Val Glu Ile Arg Ala Ile Leu His Asn
 805 810 815
 Tyr Val Asn Glu Asp Ile Tyr Val Arg Val Glu Leu Leu Tyr Asn Pro
 820 825 830
 Ala Phe Cys Ser Ala Ser Thr Lys Gly Gln Arg Tyr Arg Gln Gln Phe
 835 840 845
 Pro Ile Lys Ala Leu Ser Ser Arg Ala Val Pro Phe Val Ile Val Pro
 850 855 860
 Leu Glu Gln Gly Leu His Asp Val Glu Ile Lys Ala Ser Val Gln Glu
 865 870 875 880
 Ala Leu Trp Ser Asp Gly Val Arg Lys Lys Leu Lys Val Val Pro Glu
 885 890 895
 Gly Val Gln Lys Ser Ile Val Thr Ile Val Lys Leu Asp Pro Arg Ala
 900 905 910
 Lys Gly Val Gly Gly Thr Gln Leu Glu Val Ile Lys Ala Arg Lys Leu
 915 920 925
 Asp Asp Arg Val Pro Asp Thr Glu Ile Glu Thr Lys Ile Ile Ile Gln
 930 935 940
 Gly Asp Pro Val Ala Gln Ile Ile Glu Asn Ser Ile Asp Gly Ser Lys
 945 950 955 960
 Leu Asn His Leu Ile Thr Pro Ser Gly Cys Gly Glu Gln Asn Met
 965 970 975

Ile Arg Met Ala Ala Pro Val Ile Ala Thr Tyr Tyr Leu Asp Thr Thr
 980 985 990
 Glu Gln Trp Glu Thr Leu Gly Ile Asn Arg Arg Thr Glu Ala Val Asn
 995 1000 1005
 Gln Ile Val Thr Gly Tyr Ala Gln Gln Met Val Tyr Lys Lys Ala Asp
 1010 1015 1020
 His Ser Tyr Ala Ala Phe Thr Asn Arg Ala Ser Ser Ser Trp Leu Thr
 1025 1030 1035 1040
 Ala Tyr Val Val Lys Val Phe Ala Met Ala Ala Lys Met Val Ala Gly
 1045 1050 1055
 Ile Ser His Glu Ile Ile Cys Gly Gly Val Arg Trp Leu Ile Leu Asn
 1060 1065 1070
 Arg Gln Gln Pro Asp Gly Ala Phe Lys Glu Asn Ala Pro Val Leu Ser
 1075 1080 1085
 Gly Thr Met Gln Gly Gly Ile Gln Gly Ala Glu Glu Glu Val Tyr Leu
 1090 1095 1100
 Thr Ala Phe Ile Leu Val Ala Leu Leu Glu Ser Lys Thr Ile Cys Asn
 1105 1110 1115 1120
 Asp Tyr Val Asn Ser Leu Asp Ser Ser Ile Lys Lys Ala Thr Asn Tyr
 1125 1130 1135
 Leu Leu Lys Lys Tyr Glu Lys Leu Gln Arg Pro Tyr Thr Thr Ala Leu
 1140 1145 1150
 Thr Ala Tyr Ala Leu Ala Ala Ala Asp Gln Leu Asn Asp Asp Arg Val
 1155 1160 1165
 Leu Met Ala Ala Ser Thr Gly Arg Asp His Trp Glu Glu Tyr Asn Ala
 1170 1175 1180
 His Thr His Asn Ile Glu Gly Thr Ser Tyr Ala Leu Leu Ala Leu Leu
 1185 1190 1195 1200
 Lys Met Lys Lys Phe Asp Gln Thr Gly Pro Ile Val Arg Trp Leu Thr
 1205 1210 1215
 Asp Gln Asn Phe Tyr Gly Glu Thr Tyr Gly Gln Thr Gln Ala Thr Val
 1220 1225 1230
 Met Ala Phe Gln Ala Leu Ala Glu Tyr Glu Ile Gln Met Pro Thr His
 1235 1240 1245
 Lys Asp Leu Asn Leu Asp Ile Thr Ile Glu Leu Pro Asp Arg Glu Val
 1250 1255 1260
 Pro Ile Arg Tyr Arg Ile Asn Tyr Glu Asn Ala Leu Leu Ala Arg Thr
 1265 1270 1275 1280
 Val Glu Thr Lys Leu Asn Gln Asp Ile Thr Val Thr Ala Ser Gly Asp
 1285 1290 1295
 Gly Lys Ala Thr Met Thr Ile Leu Thr Phe Tyr Asn Ala Gln Leu Gln
 1300 1305 1310
 Glu Lys Ala Asn Val Cys Asn Lys Phe His Leu Asn Val Ser Val Glu
 1315 1320 1325
 Asn Ile His Leu Asn Ala Met Gly Ala Lys Gly Ala Leu Met Leu Lys
 1330 1335 1340
 Ile Cys Thr Arg Tyr Leu Gly Glu Val Asp Ser Thr Met Thr Ile Ile
 1345 1350 1355 1360
 Asp Ile Ser Met Leu Thr Gly Phe Leu Pro Asp Ala Glu Asp Leu Thr
 1365 1370 1375
 Arg Leu Ser Lys Gly Val Asp Arg Tyr Ile Ser Arg Tyr Glu Val Asp
 1380 1385 1390
 Asn Asn Met Ala Gln Lys Val Ala Val Ile Ile Tyr Leu Asn Lys Val
 1395 1400 1405
 Ser His Ser Glu Asp Glu Cys Leu His Phe Lys Ile Leu Lys His Phe
 1410 1415 1420
 Glu Val Gly Phe Ile Gln Pro Gly Ser Val Lys Val Tyr Ser Tyr Tyr
 1425 1430 1435 1440
 Asn Leu Asp Glu Lys Cys Thr Lys Phe Tyr His Pro Asp Lys Gly Thr
 1445 1450 1455

Gly Leu Leu Asn Lys Ile Cys Ile Gly Asn Val Cys Arg Cys Ala Gly
 1460 1465 1470
 Glu Thr Cys Ser Ser Leu Asn His Gln Glu Arg Ile Asp Val Pro Leu
 1475 1480 1485
 Gln Ile Glu Lys Ala Cys Glu Thr Asn Val Asp Tyr Val Tyr Lys Thr
 1490 1495 1500
 Lys Leu Leu Arg Ile Glu Glu Gln Asp Gly Asn Asp Ile Tyr Val Met
 1505 1510 1515 1520
 Asp Val Leu Glu Val Ile Lys Gln Gly Thr Asp Glu Asn Pro Arg Ala
 1525 1530 1535
 Lys Thr His Gln Tyr Ile Ser Gln Arg Lys Cys Gln Glu Ala Leu Asn
 1540 1545 1550
 Leu Lys Val Asn Asp Asp Tyr Leu Ile Trp Gly Ser Arg Ser Asp Leu
 1555 1560 1565
 Leu Pro Thr Lys Asp Lys Ile Ser Tyr Ile Ile Thr Lys Asn Thr Trp
 1570 1575 1580
 Ile Glu Arg Trp Pro His Glu Asp Glu Cys Gln Glu Glu Glu Phe Gln
 1585 1590 1595 1600
 Lys Leu Cys Asp Asp Phe Ala Gln Phe Ser Tyr Thr Leu Thr Glu Phe
 1605 1610 1615
 Gly Cys Pro Thr
 1620

<210> 25

<211> 3039

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 25

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 aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
 aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtagc aggaggatac 240
 aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
 aacttctcca tgaacggaaa caagtctgtt tgggtgtcaag caaataatat gtgggggccc 360
 acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
 cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact 480
 tacagctgtg aatctgggta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 540
 ggaaaatgga gtgctgtccc cccacatgt gaagaggcac gctgtaaatc tctaggacga 600
 ttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaaactt 660
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 cagggagttg cttggaccaa aatgccagta tgtgaagaaa ttttttgccc atcacctccc 780
 cctattctca atggaagaca tataggcaac tcactagcaa atgtctcata tggaagcata 840
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 aaaccccagc accaatttgt tagaccagat gtcaactctt cttgtggtga aggttacaag 1440
 ttaagtggga gtgtttatca ggagtgtcaa ggcacaattc cttgggttat ggagattcgt 1500
 ctttgtaaag aaatcacctg cccaccaccc cctgttatct acaatggggc acacaccggg 1560
 agttccttag aagattttcc atatggaacc acggtcactt acacatgtaa ccctggggcca 1620

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cagtgtcac atgtccatat tgcaaatgga tacaagatat ctggcaagga agcccatat 1800
ttctacaatg acactgtgac attcaagtgt tatagtggat ttactttgaa gggcagtagt 1860
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gctgcaggtt tgatacttct taccttcttg attgtcatta ccttatacgt gatatcaaaa 2940
cacagagaac gcaattatta tacagataca agccagaaaag aagcttttca tttagaagca 3000
cgagaagtat attctgttga tccatacaac ccagccagc 3039

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<210> 26

<211> 1033

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 26

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Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
          35          40          45
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
          50          55          60
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
          65          70          75          80
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
          85          90          95
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
          100          105          110
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
          115          120          125
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
          130          135          140
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
          145          150          155          160
His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
          165          170          175
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
          180          185          190
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
          195          200          205

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Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
 210 215 220
 Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
 225 230 235 240
 Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
 245 250 255
 Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
 260 265 270
 Glu Ile Phe Cys Pro Ser Pro Pro Ile Leu Asn Gly Arg His Ile
 275 280 285
 Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr
 290 295 300
 Cys Asp Pro Asp Pro Glu Gly Val Asn Phe Ile Leu Ile Gly Glu
 305 310 315 320
 Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser
 325 330 335
 Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro
 340 345 350
 His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg
 355 360 365
 Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr
 370 375 380
 Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu
 385 390 395 400
 Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile
 405 410 415
 Leu Asn Gly Gln Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly
 420 425 430
 Thr Ser Ile Lys Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu
 435 440 445
 Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro
 450 455 460
 Gln Cys Lys Val Ala Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr
 465 470 475 480
 Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly
 485 490 495
 Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr
 500 505 510
 Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro
 515 520 525
 Pro Pro Pro Val Ile Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu
 530 535 540
 Asp Phe Pro Tyr Gly Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro
 545 550 555 560
 Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys
 565 570 575
 Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu
 580 585 590
 Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala
 595 600 605
 Asn Gly Tyr Lys Ile Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp
 610 615 620
 Thr Val Thr Phe Lys Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser
 625 630 635 640
 Gln Ile Arg Cys Lys Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val
 645 650 655
 Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu
 660 665 670
 Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly
 675 680 685

Tyr Gln Leu Thr Gly His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn
 690 695 700
 Gly Ile Trp Phe Lys Lys Ile Pro Leu Cys Lys Val Ile His Cys His
 705 710 715 720
 Pro Pro Pro Val Ile Val Asn Gly Lys His Thr Gly Met Met Ala Glu
 725 730 735
 Asn Phe Leu Tyr Gly Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe
 740 745 750
 Tyr Leu Leu Gly Glu Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly
 755 760 765
 His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro
 770 775 780
 Val Thr Arg Cys Pro Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn
 785 790 795 800
 Lys Thr His Ser Ala Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys
 805 810 815
 Asn Pro Gly Phe Ile Met Asn Gly Ser Arg Val Ile Arg Cys His Thr
 820 825 830
 Asp Asn Thr Trp Val Pro Gly Val Pro Thr Cys Met Lys Lys Ala Phe
 835 840 845
 Ile Gly Cys Pro Pro Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly
 850 855 860
 Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys
 865 870 875 880
 Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His
 885 890 895
 Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys
 900 905 910
 Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg
 915 920 925
 Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly
 930 935 940
 Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln
 945 950 955 960
 Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val
 965 970 975
 Leu Cys Gly Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val
 980 985 990
 Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr
 995 1000 1005
 Asp Thr Ser Gln Lys Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr
 1010 1015 1020
 Ser Val Asp Pro Tyr Asn Pro Ala Ser
 1025 1030

<210> 27

<211> 3042

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 27

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 aaggctatct tttgtataag tgaaaatcaa gtgcatgccca cctggggataa agctcctcct 180
 atatgtgaat ctgtgaataa aaccatttct tgctcagatc ccatagtacc aggggggattc 240
 atgaataaag gatctaaggc accattcaga catggtgatt ctgtgacatt tacctgtaaa 300

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gccaaacttca ccatgaaagg aagcaaaact gtctgggtgcc aggcaaatga aatgtgggga 360
ccaacagctc tgccagtctg tgagagtgat ttccctctgg agtgcccatc acttccaacg 420
attcataatg gacaccacac aggacagcat gttgaccagt ttgttgctgg gttgtctgtg 480
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tcaggagact gggatgggtg catcccagaca tgcaaaaggg cccagtgtga acatccagga 600
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gagaagacta tcaattgtac tactggtagt cagaagactg ggatctggag tggccctgct 960
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cagtttaagt agagtgttga tcaactgtgt caaggtaaaa ttccttgggt tatagaaatc 1500
cgtctttgtg aagaaatcac ctgcccacca cctcctgtta tacacaacgg gacacataca 1560
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atttctgtgg gctcagcact tatcattttg atgagtgtcg gcttctgtat gatattaaaa 2940
cacagagaaa gcaattatta tacaagaca agacccaaag aaggagctct tcatttagaa 3000
acacgagaag tatattctat tgatccatat aaccagcaa gc 3042

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<210> 28

<211> 1014

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 28

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Ile Ser Cys Asp Pro Pro Pro Glu Val Lys Asn Ala Arg Lys Pro Tyr
1           5           10           15
Tyr Ser Leu Pro Ile Val Pro Gly Thr Val Leu Arg Tyr Thr Cys Ser
20           25           30

```


Pro Ser Tyr Arg Leu Ile Gly Glu Lys Ala Ile Phe Cys Ile Ser Glu
 35 40 45
 Asn Gln Val His Ala Thr Trp Asp Lys Ala Pro Pro Ile Cys Glu Ser
 50 55 60
 Val Asn Lys Thr Ile Ser Cys Ser Asp Pro Ile Val Pro Gly Gly Phe
 65 70 75 80
 Met Asn Lys Gly Ser Lys Ala Pro Phe Arg His Gly Asp Ser Val Thr
 85 90 95
 Phe Thr Cys Lys Ala Asn Phe Thr Met Lys Gly Ser Lys Thr Val Trp
 100 105 110
 Cys Gln Ala Asn Glu Met Trp Gly Pro Thr Ala Leu Pro Val Cys Glu
 115 120 125
 Ser Asp Phe Pro Leu Glu Cys Pro Ser Leu Pro Thr Ile His Asn Gly
 130 135 140
 His His Thr Gly Gln His Val Asp Gln Phe Val Ala Gly Leu Ser Val
 145 150 155 160
 Thr Tyr Ser Cys Glu Pro Gly Tyr Leu Leu Thr Gly Lys Lys Thr Ile
 165 170 175
 Lys Cys Leu Ser Ser Gly Asp Trp Asp Gly Val Ile Pro Thr Cys Lys
 180 185 190
 Glu Ala Gln Cys Glu His Pro Gly Lys Phe Pro Asn Gly Gln Val Lys
 195 200 205
 Glu Pro Leu Ser Leu Gln Val Gly Thr Thr Val Tyr Phe Ser Cys Asn
 210 215 220
 Glu Gly Tyr Gln Leu Gln Gly Gln Pro Ser Ser Gln Cys Val Ile Val
 225 230 235 240
 Glu Gln Lys Ala Ile Trp Thr Lys Lys Pro Val Cys Lys Glu Ile Leu
 245 250 255
 Cys Pro Pro Pro Pro Pro Val Arg Asn Gly Ser His Thr Gly Ser Phe
 260 265 270
 Ser Glu Asn Val Pro Tyr Gly Ser Thr Val Thr Tyr Thr Cys Asp Pro
 275 280 285
 Ser Pro Glu Lys Gly Val Ser Phe Thr Leu Ile Gly Glu Lys Thr Ile
 290 295 300
 Asn Cys Thr Thr Gly Ser Gln Lys Thr Gly Ile Trp Ser Gly Pro Ala
 305 310 315 320
 Pro Tyr Cys Val Leu Ser Thr Ser Ala Val Leu Cys Leu Gln Pro Lys
 325 330 335
 Ile Lys Arg Gly Gln Ile Leu Ser Ile Leu Lys Asp Ser Tyr Ser Tyr
 340 345 350
 Asn Asp Thr Val Ala Phe Ser Cys Glu Pro Gly Phe Thr Leu Lys Gly
 355 360 365
 Asn Arg Ser Ile Arg Cys Asn Ala His Gly Thr Trp Glu Pro Pro Val
 370 375 380
 Pro Val Cys Glu Lys Gly Cys Gln Ala Pro Pro Lys Ile Ile Asn Gly
 385 390 395 400
 Gln Lys Glu Asp Ser Tyr Leu Leu Asn Phe Asp Pro Gly Thr Ser Ile
 405 410 415
 Arg Tyr Ser Cys Asp Pro Gly Tyr Leu Leu Val Gly Glu Asp Thr Ile
 420 425 430
 His Cys Thr Pro Glu Gly Lys Trp Thr Pro Ile Thr Pro Gln Cys Thr
 435 440 445
 Val Ala Glu Cys Lys Pro Val Gly Pro His Leu Phe Lys Arg Pro Gln
 450 455 460
 Asn Gln Phe Ile Arg Thr Ala Val Asn Ser Ser Cys Asp Glu Gly Phe
 465 470 475 480
 Gln Leu Ser Glu Ser Ala Tyr Gln Leu Cys Gln Gly Thr Ile Pro Trp
 485 490 495
 Phe Ile Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro Pro Pro Pro
 500 505 510

Val Ile His Asn Gly Thr His Thr Trp Ser Ser Ser Glu Asp Val Pro
 515 520 525
 Tyr Gly Thr Val Val Thr Tyr Met Cys Tyr Pro Gly Pro Glu Glu Gly
 530 535 540
 Val Lys Phe Lys Leu Ile Gly Glu Gln Thr Ile His Cys Thr Ser Asp
 545 550 555 560
 Ser Arg Gly Arg Gly Ser Trp Ser Ser Pro Ala Pro Leu Cys Lys Leu
 565 570 575
 Ser Leu Pro Ala Val Gln Cys Thr Asp Val His Val Glu Asn Gly Val
 580 585 590
 Lys Leu Thr Asp Asn Lys Ala Pro Tyr Phe Tyr Asn Asp Ser Val Met
 595 600 605
 Phe Lys Cys Asp Asp Gly Tyr Ile Leu Ser Gly Ser Ser Gln Ile Arg
 610 615 620
 Cys Lys Ala Asn Asn Thr Trp Asp Pro Glu Lys Pro Leu Cys Lys Lys
 625 630 635 640
 Glu Gly Cys Glu Pro Met Arg Val His Gly Leu Pro Asp Asp Ser His
 645 650 655
 Ile Lys Leu Val Lys Arg Thr Cys Gln Asn Gly Tyr Gln Leu Thr Gly
 660 665 670
 Tyr Thr Tyr Glu Lys Cys Gln Asn Ala Glu Asn Gly Thr Trp Phe Lys
 675 680 685
 Lys Ile Glu Val Cys Thr Val Ile Leu Cys Gln Pro Pro Pro Lys Ile
 690 695 700
 Ala Asn Gly Gly His Thr Gly Met Met Ala Lys His Phe Leu Tyr Gly
 705 710 715 720
 Asn Glu Val Ser Tyr Glu Cys Asp Glu Gly Phe Tyr Leu Leu Gly Glu
 725 730 735
 Lys Ser Leu Gln Cys Val Asn Asp Ser Lys Gly His Gly Ser Trp Ser
 740 745 750
 Gly Pro Pro Pro Gln Cys Leu Gln Ser Ser Pro Leu Thr His Cys Pro
 755 760 765
 Asp Pro Glu Val Lys His Gly Tyr Lys Leu Asn Lys Thr His Ser Ala
 770 775 780
 Phe Ser His Asn Asp Ile Val His Phe Val Cys Asn Gln Gly Phe Ile
 785 790 795 800
 Met Asn Gly Ser His Leu Ile Arg Cys His Thr Asn Asn Thr Trp Leu
 805 810 815
 Pro Gly Val Pro Thr Cys Ile Arg Lys Ala Ser Leu Gly Cys Gln Ser
 820 825 830
 Pro Ser Thr Ile Pro Asn Gly Asn His Thr Gly Gly Ser Ile Ala Arg
 835 840 845
 Phe Pro Pro Gly Met Ser Val Met Tyr Ser Cys Tyr Gln Gly Phe Leu
 850 855 860
 Met Ala Gly Glu Ala Arg Leu Ile Cys Thr His Glu Gly Thr Trp Ser
 865 870 875 880
 Gln Pro Pro Pro Phe Cys Lys Glu Val Asn Cys Ser Phe Pro Glu Asp
 885 890 895
 Thr Asn Gly Ile Gln Lys Gly Phe Gln Pro Gly Lys Thr Tyr Arg Phe
 900 905 910
 Gly Ala Thr Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly
 915 920 925
 Ser Pro Gln Ser Gln Cys Gln Asp Asp Ser Gln Trp Asn Pro Pro Leu
 930 935 940
 Ala Leu Cys Lys Tyr Arg Arg Trp Ser Thr Ile Pro Leu Ile Cys Gly
 945 950 955 960
 Ile Ser Val Gly Ser Ala Leu Ile Ile Leu Met Ser Val Gly Phe Cys
 965 970 975
 Met Ile Leu Lys His Arg Glu Ser Asn Tyr Tyr Thr Lys Thr Arg Pro
 980 985 990

Lys Glu Gly Ala Leu His Leu Glu Thr Arg Glu Val Tyr Ser Ile Asp
 995 1000 1005
 Pro Tyr Asn Pro Ala Ser
 1010

<210> 29
 <211> 1033
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

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 20 25 30
 Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
 35 40 45
 Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
 50 55 60
 Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
 65 70 75 80
 Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
 85 90 95
 Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
 100 105 110
 Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
 115 120 125
 Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
 130 135 140
 Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
 145 150 155 160
 His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
 165 170 175
 Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
 180 185 190
 Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
 195 200 205
 Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
 210 215 220
 Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
 225 230 235 240
 Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
 245 250 255
 Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
 260 265 270
 Glu Ile Phe Cys Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile
 275 280 285
 Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr
 290 295 300
 Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu
 305 310 315 320
 Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser
 325 330 335
 Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro
 340 345 350

His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg
 355 360 365
 Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr
 370 375 380
 Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu
 385 390 395 400
 Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile
 405 410 415
 Leu Asn Gly Gln Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly
 420 425 430
 Thr Ser Ile Lys Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu
 435 440 445
 Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro
 450 455 460
 Gln Cys Lys Val Ala Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr
 465 470 475 480
 Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly
 485 490 495
 Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr
 500 505 510
 Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro
 515 520 525
 Pro Pro Pro Val Ile Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu
 530 535 540
 Asp Phe Pro Tyr Gly Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro
 545 550 555 560
 Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys
 565 570 575
 Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu
 580 585 590
 Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala
 595 600 605
 Asn Gly Tyr Lys Ile Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp
 610 615 620
 Thr Val Thr Phe Lys Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser
 625 630 635 640
 Gln Ile Arg Cys Lys Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val
 645 650 655
 Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu
 660 665 670
 Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly
 675 680 685
 Tyr Gln Leu Thr Gly His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn
 690 695 700
 Gly Ile Trp Phe Lys Lys Ile Pro Leu Cys Lys Val Ile His Cys His
 705 710 715 720
 Pro Pro Pro Val Ile Val Asn Gly Lys His Thr Gly Met Met Ala Glu
 725 730 735
 Asn Phe Leu Tyr Gly Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe
 740 745 750
 Tyr Leu Leu Gly Glu Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly
 755 760 765
 His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro
 770 775 780
 Val Thr Arg Cys Pro Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn
 785 790 795 800
 Lys Thr His Ser Ala Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys
 805 810 815
 Asn Pro Gly Phe Ile Met Asn Gly Ser Arg Val Ile Arg Cys His Thr
 820 825 830

Asp Asn Thr Trp Val Pro Gly Val Pro Thr Cys Met Lys Lys Ala Phe
 835 840 845
 Ile Gly Cys Pro Pro Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly
 850 855 860
 Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys
 865 870 875 880
 Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His
 885 890 895
 Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys
 900 905 910
 Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg
 915 920 925
 Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly
 930 935 940
 Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln
 945 950 955 960
 Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val
 965 970 975
 Leu Cys Gly Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val
 980 985 990
 Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr
 995 1000 1005
 Asp Thr Ser Gln Lys Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr
 1010 1015 1020
 Ser Val Asp Pro Tyr Asn Pro Ala Ser
 1025 1030